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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/075,074

DATE: 03/01/2002 8:55
TIME: 11:45:05

Input Set : A:\EP.txt
Output Set: N:\CRF3\03012002\J075074.raw

3 <110> APPLICANT: Brown, Arthur
 4 Wible, Barbara
 5 Yang, Qing
 7 <120> TITLE OF INVENTION: Protein That Enhances Expression of Potassium Channels on
 Cell Surfaces
 8 and Nucleic Acids That Encode The Same
 10 <130> FILE REFERENCE: 22884/04066
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/075,074
 C--> 12 <141> CURRENT FILING DATE: 2002-12-13
 12 <150> PRIOR APPLICATION NUMBER: 09/062,440
 13 <151> PRIOR FILING DATE: 1998-04-17
 15 <150> PRIOR APPLICATION NUMBER: 09/712,495
 16 <151> PRIOR FILING DATE: 2000-11-14
 18 <160> NUMBER OF SEQ ID NOS: 13
 20 <170> SOFTWARE: PatentIn version 3.0
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1725
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Rattus norvegicus
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (1)..(1725)
 31 <400> SEQUENCE: 1
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 33 Met Lys Ile Lys Glu Leu Tyr Arg Arg Arg Phe Pro Arg Lys Thr Leu
 34 1 5 10 15
 36 ggg cct tcc gat ctc tct ttg ctc tct ttg ccc cct ggc acc tct cct 96
 37 Gly Pro Ser Asp Leu Ser Leu Ser Leu Pro Pro Gly Thr Ser Pro
 38 20 25 30
 40 gta ggc tcc ccc agc ccc ctt gct tcc att cct ccc acc ctc ctg acc 144
 41 Val Gly Ser Pro Ser Pro Leu Ala Ser Ile Pro Pro Thr Leu Leu Thr
 42 35 40 45
 44 cct ggc acc ttg ctg ggc cct aag cgt gag gtg gac atg cac cct cct 192
 45 Pro Gly Thr Leu Leu Gly Pro Lys Arg Glu Val Asp Met His Pro Pro
 46 50 55 60
 48 ctg ccc cag cct gtg cac cct gac gtc acc atg aaa cca ctg ccc ttc 240
 49 Leu Pro Gln Pro Val His Pro Asp Val Thr Met Lys Pro Leu Pro Phe
 50 65 70 75 80
 52 tac gaa gtc tac gga gag ctc atc cgg ccg acc acc ctt gcg tcc acc 288
 53 Tyr Glu Val Tyr Gly Glu Leu Ile Arg Pro Thr Thr Leu Ala Ser Thr
 54 85 90 95
 56 tcc agt cag agg ttt gag gaa gcc cac ttt acc ttt gca ctc act ccc 336
 57 Ser Ser Gln Arg Phe Glu Ala His Phe Thr Phe Ala Leu Thr Pro
 58 100 105 110

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60	cag	cag	ctg	cag	cag	att	ctc	aca	tcc	agg	gag	gtt	ctg	cca	gga	gcc	384
61	Gln	Gln	Leu	Gln	Gln	Ile	Leu	Thr	Ser	Arg	Glu	Val	Leu	Pro	Gly	Ala	
62	115					120				125							
64	aag	tgc	gat	tat	acc	ata	caa	gtg	cag	ctc	agg	ttc	tgt	ctc	tgt	gag	432
65	Lys	Cys	Asp	Tyr	Thr	Ile	Gln	Val	Gln	Leu	Arg	Phe	Cys	Leu	Cys	Glu	
66	130					135				140							
68	acc	agc	tgc	ccc	cag	gag	gac	tat	ttc	ccc	cct	aac	ctc	ttt	gtc	aag	480
69	Thr	Ser	Cys	Pro	Gln	Glu	Asp	Tyr	Phe	Pro	Pro	Asn	Leu	Phe	Val	Lys	
70	145					150				155				160			
72	gtt	aat	ggg	aaa	ctc	tgc	ccc	ctg	ccg	ggt	tac	ctc	cct	cca	acc	aag	528
73	Val	Asn	Gly	Lys	Leu	Cys	Pro	Leu	Pro	Gly	Tyr	Leu	Pro	Pro	Thr	Lys	
74						165			170			175					
76	aat	gga	gct	gag	ccc	aag	agg	cct	agt	cgt	cca	atc	aac	atc	aca	ccc	576
77	Asn	Gly	Ala	Glu	Pro	Lys	Arg	Pro	Ser	Arg	Pro	Ile	Asn	Ile	Thr	Pro	
78						180			185			190					
80	ctg	gct	cgt	ctc	tca	gcc	act	gtt	ccc	aac	acc	ata	gtg	gtt	aac	tgg	624
81	Leu	Ala	Arg	Leu	Ser	Ala	Thr	Val	Pro	Asn	Thr	Ile	Val	Val	Asn	Trp	
82						195			200			205					
84	tca	tct	gag	ttt	gga	cgg	aat	tac	tcc	ttg	tct	gtg	tac	ctg	gtg	agg	672
85	Ser	Ser	Glu	Phe	Gly	Arg	Asn	Tyr	Ser	Leu	Ser	Val	Tyr	Leu	Val	Arg	
86						210			215			220					
88	cag	ttg	act	gca	ggg	acc	ctg	cta	caa	aag	ctc	aga	gcc	aag	ggt	atc	720
89	Gln	Leu	Thr	Ala	Gly	Thr	Leu	Leu	Gln	Lys	Leu	Arg	Ala	Lys	Gly	Ile	
90	225					230			235			240					
92	cgg	aat	cca	gac	cat	tcc	cga	gca	ctg	atc	aag	gag	aaa	ttg	act	gct	768
93	Arg	Asn	Pro	Asp	His	Ser	Arg	Ala	Leu	Ile	Lys	Glu	Lys	Leu	Thr	Ala	
94						245			250			255					
96	gac	ccc	gac	agt	gaa	gtg	gct	act	aca	agt	ctc	ccg	gtg	tca	ctc	atg	816
97	Asp	Pro	Asp	Ser	Glu	Val	Ala	Thr	Ser	Leu	Arg	Val	Ser	Leu	Met		
98						260			265			270					
100	tgc	ccg	ctg	ggg	aag	atg	cgc	ctg	act	gtc	cca	tgc	cgc	gct	ctc	acc	864
101	Cys	Pro	Leu	Gly	Lys	Met	Arg	Leu	Thr	Val	Pro	Cys	Arg	Ala	Leu	Thr	
102						275			280			285					
104	tgt	gcc	cac	ctg	cag	agt	ttc	gat	gct	gcc	ctt	tat	cta	cag	atg	aat	912
105	Cys	Ala	His	Leu	Gln	Ser	Phe	Asp	Ala	Ala	Leu	Tyr	Leu	Gln	Met	Asn	
106						290			295			300					
108	gag	aaa	aag	cca	aca	tgg	acg	tgc	cct	gtg	tgt	gac	aag	aag	gct	ccc	960
109	Glu	Lys	Lys	Pro	Thr	Trp	Thr	Cys	Pro	Val	Cys	Asp	Lys	Lys	Ala	Pro	
110						305			310			315			320		
112	tat	gag	tca	ctg	att	att	gat	ggt	tta	ttc	atg	gaa	att	ctt	aat	tcc	1008
113	Tyr	Glu	Ser	Leu	Ile	Ile	Asp	Gly	Leu	Phe	Met	Glu	Ile	Leu	Asn	Ser	
114						325			330			335					
116	tgt	tgc	gat	tgt	gat	gag	atc	cag	ttc	atg	gaa	gat	gga	tcc	tgg	tgt	1056
117	Cys	Ser	Asp	Cys	Asp	Glu	Ile	Gln	Phe	Met	Glu	Asp	Gly	Ser	Trp	Cys	
118						340			345			350					
120	cca	atg	aaa	ccc	aag	aag	gag	gca	tcc	gag	gtt	ctg	ccc	cca	cca	ggg	1104
121	Pro	Met	Lys	Pro	Lys	Lys	Glu	Ala	Ser	Glu	Val	Cys	Pro	Pro	Pro	Gly	
122						355			360			365					
124	tat	ggg	ctg	gat	ggt	ctc	cag	tat	agc	cca	gtc	cag	gag	gga	aat	cag	1152

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125	Tyr	Gly	Leu	Asp	Gly	Leu	Gln	Tyr	Ser	Pro	Val	Gln	Glu	Gly	Asn	Gln	
126	370					375						380					
128	tca	gag	aat	aag	aag	agg	gtt	gaa	gtc	att	gac	ttg	aca	atc	gaa	agc	1200
129	Ser	Glu	Asn	Lys	Lys	Arg	Val	Glu	Val	Ile	Asp	Leu	Thr	Ile	Glu	Ser	
130	385					390						395				400	
132	tca	tca	gat	gag	gaa	gat	ctg	ccc	ccc	acc	aag	cac	tgc	cct	gtt		1248
133	Ser	Ser	Asp	Glu	Glu	Asp	Leu	Pro	Pro	Thr	Lys	Lys	His	Cys	Pro	Val	
134						405					410				415		
136	acc	tcg	gct	gcc	att	cca	gcc	ctt	cct	gga	agc	aaa	gga	gcc	ctg	acc	1296
137	Thr	Ser	Ala	Ala	Ile	Pro	Ala	Leu	Pro	Gly	Ser	Lys	Gly	Ala	Leu	Thr	
138						420					425				430		
140	tct	ggt	cac	cag	ccg	tct	tcg	gtg	ctg	cg	agc	cct	gca	atg	gg	aca	1344
141	Ser	Gly	His	Gln	Pro	Ser	Ser	Val	Leu	Arg	Ser	Pro	Ala	Met	Gly	Thr	
142						435					440				445		
144	ctg	ggc	agt	gat	tcc	ctg	tct	agt	ctc	cca	cta	cat	gag	tac	cca	cct	1392
145	Leu	Gly	Ser	Asp	Phe	Leu	Ser	Ser	Leu	Pro	Leu	His	Glu	Tyr	Pro	Pro	
146						450					455				460		
148	gcc	ttc	ccg	ctg	ggg	gct	gac	atc	caa	gg	tta	gat	tta	ttt	tct	ttc	1440
149	Ala	Phe	Pro	Leu	Gly	Ala	Asp	Ile	Gln	Gly	Leu	Asp	Leu	Phe	Ser	Phe	
150						465					470				475		
152	ctt	cag	act	gag	agt	cag	cac	tac	agc	cct	tca	gtt	atc	act	tca	cta	1488
153	Leu	Gln	Thr	Glu	Ser	Gln	His	Tyr	Ser	Pro	Ser	Val	Ile	Thr	Ser	Leu	
154						485					490				495		
156	gat	gag	cag	gac	acc	ctt	ggc	cac	tcc	ttc	caa	ttc	cg	gga	acc	cct	1536
157	Asp	Glu	Gln	Asp	Thr	Leu	Gly	His	Phe	Phe	Gln	Phe	Arg	Gly	Thr	Pro	
158						500					505				510		
160	ccc	cac	tcc	ctg	ggc	cca	ctg	gcc	ccc	aca	ttg	ggg	agc	tct	cac	cgc	1584
161	Pro	His	Phe	Leu	Gly	Pro	Leu	Ala	Pro	Thr	Leu	Gly	Ser	Ser	His	Arg	
162						515					520				525		
164	agc	gcc	act	cca	gca	ccc	gct	cct	ggc	cgt	gtc	agc	agc	att	gtg	gct	1632
165	Ser	Ala	Thr	Pro	Ala	Pro	Ala	Pro	Gly	Arg	Val	Ser	Ser	Ile	Val	Ala	
166						530					535				540		
168	cct	ggg	agt	tcc	ttg	agg	gaa	ggg	cat	gga	gga	ccc	ctg	cct	tcc	gg	1680
169	Pro	Gly	Ser	Ser	Leu	Arg	Glu	Gly	His	Gly	Gly	Pro	Leu	Pro	Ser	Gly	
170						545					550				555		
172	ccc	tct	ttg	act	ggc	tgt	cg	tca	gac	gtc	att	tcc	ttg	gac	tga		1725
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178	<211>	LENGTH:	574														
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188	Gly	Pro	Ser	Asp	Leu	Ser	Leu	Leu	Ser	Leu	Pro	Pro	Gly	Thr	Ser	Pro	
189					20						25				30		
192	Val	Gly	Ser	Pro	Ser	Pro	Leu	Ala	Ser	Ile	Pro	Pro	Thr	Leu	Leu	Thr	
193					35						40				45		

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196 Pro Gly Thr Leu Leu Gly Pro Lys Arg Glu Val Asp Met His Pro Pro
197 50 55 60
200 Leu Pro Gln Pro Val His Pro Asp Val Thr Met Lys Pro Leu Pro Phe
201 65 70 75 80
204 Tyr Glu Val Tyr Gly Glu Leu Ile Arg Pro Thr Thr Leu Ala Ser Thr
205 85 90 95
208 Ser Ser Gln Arg Phe Glu Glu Ala His Phe Thr Phe Ala Leu Thr Pro
209 100 105 110
212 Gln Gln Leu Gln Gln Ile Leu Thr Ser Arg Glu Val Leu Pro Gly Ala
213 115 120 125
216 Lys Cys Asp Tyr Thr Ile Gln Val Gln Leu Arg Phe Cys Leu Cys Glu
217 130 135 140
220 Thr Ser Cys Pro Gln Glu Asp Tyr Phe Pro Pro Asn Leu Phe Val Lys
221 145 150 155 160
224 Val Asn Gly Lys Leu Cys Pro Leu Pro Gly Tyr Leu Pro Pro Thr Lys
225 165 170 175
228 Asn Gly Ala Glu Pro Lys Arg Pro Ser Arg Pro Ile Asn Ile Thr Pro
229 180 185 190
232 Leu Ala Arg Leu Ser Ala Thr Val Pro Asn Thr Ile Val Val Asn Trp
233 195 200 205
236 Ser Ser Glu Phe Gly Arg Asn Tyr Ser Leu Ser Val Tyr Leu Val Arg
237 210 215 220
240 Gln Leu Thr Ala Gly Thr Leu Leu Gln Lys Leu Arg Ala Lys Gly Ile
241 225 230 235 240
244 Arg Asn Pro Asp His Ser Arg Ala Leu Ile Lys Glu Lys Leu Thr Ala
245 245 250 255
248 Asp Pro Asp Ser Glu Val Ala Thr Thr Ser Leu Arg Val Ser Leu Met
249 260 265 270
252 Cys Pro Leu Gly Lys Met Arg Leu Thr Val Pro Cys Arg Ala Leu Thr
253 275 280 285
256 Cys Ala His Leu Gln Ser Phe Asp Ala Ala Leu Tyr Leu Gln Met Asn
257 290 295 300
260 Glu Lys Lys Pro Thr Trp Thr Cys Pro Val Cys Asp Lys Lys Ala Pro
261 305 310 315 320
264 Tyr Glu Ser Leu Ile Ile Asp Gly Leu Phe Met Glu Ile Leu Asn Ser
265 325 330 335
268 Cys Ser Asp Cys Asp Glu Ile Gln Phe Met Glu Asp Gly Ser Trp Cys
269 340 345 350
272 Pro Met Lys Pro Lys Lys Glu Ala Ser Glu Val Cys Pro Pro Pro Gly
273 355 360 365
276 Tyr Gly Leu Asp Gly Leu Gln Tyr Ser Pro Val Gln Glu Gly Asn Gln
277 370 375 380
280 Ser Glu Asn Lys Lys Arg Val Glu Val Ile Asp Leu Thr Ile Glu Ser
281 385 390 395 400
284 Ser Ser Asp Glu Glu Asp Leu Pro Pro Thr Lys Lys His Cys Pro Val
285 405 410 415
288 Thr Ser Ala Ala Ile Pro Ala Leu Pro Gly Ser Lys Gly Ala Leu Thr
289 420 425 430
292 Ser Gly His Gln Pro Ser Ser Val Leu Arg Ser Pro Ala Met Gly Thr

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293	435	440	445														
296	Leu	Gly	Ser	Asp	Phe	Leu	Ser	Ser	Leu	Pro	Leu	His	Glu	Tyr	Pro	Pro	
297	450															460	
300	Ala	Phe	Pro	Leu	Gly	Ala	Asp	Ile	Gln	Gly	Leu	Asp	Leu	Phe	Ser	Phe	
301	465															475	
304	Leu	Gln	Thr	Glu	Ser	Gln	His	Tyr	Ser	Pro	Ser	Val	Ile	Thr	Ser	Leu	
305																495	
308	Asp	Glu	Gln	Asp	Thr	Leu	Gly	His	Phe	Phe	Gln	Phe	Arg	Gly	Thr	Pro	
309																510	
312	Pro	His	Phe	Leu	Gly	Pro	Leu	Ala	Pro	Thr	Leu	Gly	Ser	Ser	His	Arg	
313																525	
316	Ser	Ala	Thr	Pro	Ala	Pro	Ala	Pro	Gly	Arg	Val	Ser	Ser	Ile	Val	Ala	
317																540	
320	Pro	Gly	Ser	Ser	Leu	Arg	Glu	Gly	His	Gly	Gly	Pro	Leu	Pro	Ser	Gly	
321	545															560	
324	Pro	Ser	Leu	Thr	Gly	Cys	Arg	Ser	Asp	Val	Ile	Ser	Leu	Asp			
325																570	
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329	<211>	LENGTH:	1725														
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331	<213>	ORGANISM:	Homo sapiens														
333	<220>	FEATURE:															
334	<221>	NAME/KEY:	CDS														
335	<222>	LOCATION:	(1)..(1725)														
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340	1															15	
342	ggg	ccc	tct	gat	ctc	tcc	ctc	tct	ttg	ccc	cct	ggc	acc	tct	cct		96
343	Gly	Pro	Ser	Asp	Leu	Ser	Leu	Leu	Ser	Leu	Pro	Pro	Gly	Thr	Ser	Pro	
344																30	
346	gta	ggc	tcc	cct	ggt	cct	cta	gct	ccc	att	ccc	cca	acg	ctg	ttg	gcc	144
347	Val	Gly	Ser	Pro	Gly	Pro	Leu	Ala	Pro	Ile	Pro	Pro	Thr	Leu	Leu	Ala	
348																45	
350	cct	ggc	acc	ctg	ctg	ggc	ccc	aag	cgt	gag	gtg	gac	atg	cac	ccc	cct	192
351	Pro	Gly	Thr	Leu	Leu	Gly	Pro	Lys	Arg	Glu	Val	Asp	Met	His	Pro	Pro	
352																60	
354	ctg	ccc	cag	cct	gtg	cac	cct	gat	gtc	acc	atg	aaa	cca	ttg	ccc	ttc	240
355	Leu	Pro	Gln	Pro	Val	His	Pro	Asp	Val	Thr	Met	Lys	Pro	Leu	Pro	Phe	
356	65															80	
358	tat	gaa	gtc	tat	ggg	gag	ctc	atc	cgg	ccc	acc	acc	ctt	gca	tcc	act	288
359	Tyr	Glu	Val	Tyr	Gly	Glu	Leu	Ile	Arg	Pro	Thr	Thr	Leu	Ala	Ser	Thr	
360																95	
362	tct	agc	cag	cg	ttt	gag	gaa	g	cg	cac	ttt	gcc	ctc	aca	ccc		336
363	Ser	Ser	Gln	Arg	Phe	Glu	Glu	Ala	His	Phe	Thr	Phe	Ala	Leu	Thr	Pro	
364																110	
366	cag	caa	gtg	cag	cag	att	ctt	aca	tcc	aga	gag	gtt	ctg	cca	gga	gcc	384
367	Gln	Gln	Val	Gln	Gln	Ile	Leu	Thr	Ser	Arg	Glu	Val	Leu	Pro	Gly	Ala	
368																125	

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY DATE: 03/01/2002
PATENT APPLICATION: US/10/075,074 TIME: 11:45:06

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:795 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:810 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:849 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:858 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:861 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:864 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:867 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:873 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
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